OIPE

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    3 <110> APPLICANT: Marks, Daniel L.
    4          Cone, Roger D.
    6 <120> TITLE OF INVENTION: Methods and Reagents for Discovering and Using
    7          Mammalian Melanocortin Receptor Antagonists to Treat
    8          Cachexia
   10 <130> FILE REFERENCE: 96-886
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/074,754
C--> 13 <141> CURRENT FILING DATE: 2002-02-13
   15 <160> NUMBER OF SEQ ID NOS: 10
   17 <170> SOFTWARE: PatentIn Ver. 2.0
   19 <210> SEQ ID NO: 1
   20 <211> LENGTH: 1671
   21 <212> TYPE: DNA
   22 <213> ORGANISM: Homo sapiens
   24 <220> FEATURE:
   25 <221> NAME/KEY: CDS
   26 <222> LOCATION: (394)..(1389)
   28 <400> SEQUENCE: 1
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   33 agtgagaaca agaaagcaaa gagcagactc tttcaactga gaatgaatat tttgaagccc 180
   35 aagattttaa cgtgatgatg attagagtcg tacctaaaag agactaaaaa ctccatgtca 240
   37 agtctggac ttgtgacatt tactcacagc aggcatggca attttagcct cacaactttc 300
   39 agacagataa agacttggag gaaataactg agacgactcc ctgacccagg aggttaaatc 360
   41 aattcagggg gacactggaa ttctcctgcc agc atg gtg aac tcc acc cac cgt 414
   42                                    Met Val Asn Ser Thr His Arg
   43                                      1               5
   45 ggg atg cac act tct ctg cac ctc tgg aac cgc agc agt tac aga ctg    462
   46 Gly Met His Thr Ser Leu His Leu Trp Asn Arg Ser Ser Tyr Arg Leu
   47       10                  15                  20
   49 cac agc aat gcc agt gag tcc ctt gga aaa ggc tac tct gat gga ggg    510
   50 His Ser Asn Ala Ser Glu Ser Leu Gly Lys Gly Tyr Ser Asp Gly Gly
   51       25                  30                  35
   53 tgc tac acg caa ctt ttt gtc tct cct gag gtg ttt gtg act ctg ggt    558
   54 Cys Tyr Ala Gln Leu Phe Val Ser Pro Glu Val Phe Val Thr Leu Gly
   55    40                  45                  50                  55
   57 gtg atc agc ttg ttg gag aat atc tta gga att gtg gca ata gcc aag    606
   58 Val Ile Ser Leu Leu Glu Asn Ile Leu Glu Ile Val Ala Ile Ala Lys
   59             60                  65                  70
   61 aac aag aat ctg cat tca ccc atg tac ttt ttc atc tgc agc ttg gct    654
   62 Asn Lys Asn Leu His Ser Pro Met Tyr Phe Phe Ile Cys Ser Leu Ala
   63                  75                  80                  85
   65 gtg gct gat atg ctg gtg agc gtt tca aat gga tca gaa acc att atc    702
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file://C:\CRF4\Outhold\VsrJ074754.htm                                    10/2/02
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                    PATENT APPLICATION:  US/10/074,754   TIME: 09:45:54

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                    Output Set: N:\CRF4\10022002\J074754.raw


66 Val Ala Asp Met Leu Val Ser Val Ser Asn Gly Ser Glu Thr Ile Ile
67      90                  95                  100
69 atc acc cta tta aac cgt aca gat acg gat gca cag agt ttc aca gtg    750
70 Ile Thr Leu Leu Asn Arg Thr Asp Thr Asp Ala Gln Ser Phe Thr Val
71      105                 110                 115
73 aat att gat aat gtc att gac tcg gtg atc tgt agc tcc ttg ctt gca    798
74 Asn Ile Asp Asn Val Ile Asp Ser Val Ile Cys Ser Ser Leu Leu Ala
75 120                 125                 130                 135
77 tcc att tgc agc ctg ctt tca att gca gtg gac agg tac ttt act atc    846
78 Ser Ile Cys Ser Leu Leu Ser Ile Ala Val Asp Arg Tyr Phe Thr Ile
79              140                 145                 150
81 ttc tat gct ctc cag tac cat aac att atg aca gat aag cgg gtt ggg    894
82 Phe Tyr Ala Leu Gln Tyr His Asn Ile Met Thr Val Lys Arg Val Gly
83              155                 160                 165
85 atc agc ata agt tgt atc tgg gca gtc tgc acg gtt tca ggt att ttg    942
86 Ile Ser Ile Ser Cys Ile Trp Ala Val Cys Thr Val Ser Gly Ile Leu
87          170                 175                 180
89 ttc atc att tac tca gat agt agt gct gtc atc atc tgc ctc atc acc    990
90 Phe Ile Ile Tyr Ser Asp Ser Ser Ala Val Ile Ile Cys Leu Ile Thr
91          185                 190                 195
93 atg ttc ttc acc atg ctg gct ctc tct gtc ctc tat gtc cac gtg       1038
94 Met Phe Phe Thr Met Leu Ala Leu Ser Leu Tyr Val His Leu
95 200                 205                 210                 215
97 ttc ctg atg gcc agg ctt cac att aag agg att gct gtc ctc ccc ggc   1086
98 Phe Leu Met Ala Arg Leu His Ile Lys Arg Ile Ala Val Leu Pro Gly
99          220                 225                 230
101 act ggt gcc atc cgc caa ggt gcc aat atg aag gga gcg att acc ttg  1134
102 Thr Gly Ala Ile Arg Gln Gly Ala Asn Met Lys Gly Ala Ile Thr Leu
103             235                 240                 245
105 acc atc ctg att ggc gtc ttt gtt gtc tgc tgg gcc cca ttc ttc ctc  1182
106 Thr Ile Leu Ile Gly Val Phe Val Val Cys Trp Ala Pro Phe Phe Leu
107             250                 255                 260
109 cac tta ata ttc tac atc tct tgt cct cag aat cca tat tgt gtg tgc  1230
110 His Leu Ile Phe Tyr Ile Ser Cys Pro Gln Asn Pro Tyr Cys Val Cys
111             265                 270                 275
113 ttc atg tct cac ttt aac ttg tat ctc ata ctg atc atg tgt aat tca  1278
114 Phe Met Ser His Phe Asn Leu Tyr Leu Ile Leu Ile Met Cys Asn Ser
115 280                 285                 290                 295
117 atc gat cct ctg att tat gca ctc cgg agt caa gaa ctg agg aaa      1326
118 Ile Ile Asp Pro Leu Ile Tyr Ala Leu Arg Ser Gln Glu Leu Arg Lys
119             300                 305                 310
121 acc ttc aaa gag atc tct tcc tat ccc ctg gga ggc ctt tgt gac      1374
122 Thr Phe Lys Glu Ile Ser Ser Tyr Pro Leu Gly Gly Leu Cys Asp
123             315                 320                 325
125 ttg tct agc aga tat taaatgggga cagagcacgc aatataggaa catccataag 1429
126 Leu Ser Ser Arg Tyr
127             330
129 agacttttc actcttaccc tacctgaata ttctacttct gcaacagctt tctcttccgt 1489
131 gtagggtact ggttgagata tccattgtgt aaatttaagc ctatgatttt taatgagaaa 1549
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Input Set : A:\96886-L.seq.txt
Output Set: N:\CRF4\10022002\J074754.raw

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133 aaatgcccag tctctgtatt atttccaatc tcatgctact tttttggcca taaaatatga 1609
135 atctatgtta taggttgtag gcactgtgga tttacaaaaa gaaaagtcct tattaaaaga 1669
137 tt                                                                 1671
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141 <211> LENGTH: 332
142 <212> TYPE: PRT
143 <213> ORGANISM: Homo sapiens
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146 Met Val Asn Ser Thr His Arg Gly Met His Thr Ser Leu His Leu Trp
147  1               5                  10                  15
149 Asn Arg Ser Ser Tyr Arg Leu His Ser Asn Ala Ser Glu Ser Leu Gly
150             20                  25                  30
152 Lys Gly Tyr Ser Asp Gly Gly Cys Tyr Ala Gln Leu Phe Val Ser Pro
153         35                  40                  45
155 Glu Val Phe Val Thr Leu Gly Val Ile Ser Leu Leu Glu Asn Ile Leu
156     50                  55                  60
158 Glu Ile Val Ala Ile Ala Lys Asn Lys Asn Leu His Ser Pro Met Tyr
159  65                  70                  75                  80
161 Phe Phe Ile Cys Ser Leu Ala Val Ala Asp Met Leu Val Ser Val Ser
162                 85                  90                  95
164 Asn Gly Ser Glu Thr Ile Ile Ile Thr Leu Leu Asn Arg Thr Asp Thr
165             100                 105                 110
167 Asp Ala Gln Ser Phe Thr Val Asn Ile Asp Asn Val Ile Asp Ser Val
168         115                 120                 125
170 Ile Cys Ser Ser Leu Leu Ala Ser Ile Cys Ser Leu Ser Ile Ala
171 130                 135                 140
173 Val Asp Arg Tyr Phe Thr Ile Phe Tyr Ala Leu Gln Tyr His Asn Ile
174 145                 150                 155                 160
176 Met Thr Val Lys Arg Val Gly Ile Ser Ile Ser Cys Ile Trp Ala Ala
177                 165                 170                 175
179 Cys Thr Val Ser Gly Ile Leu Phe Ile Ile Tyr Ser Asp Ser Ser Ala
180             180                 185                 190
182 Val Ile Ile Cys Leu Ile Thr Met Phe Phe Thr Met Leu Ala Leu Met
183             195                 200                 205
185 Ala Ser Leu Tyr Val His Met Phe Leu Met Ala Arg Leu His Ile Lys
186         210                 215                 220
188 Arg Ile Ala Val Leu Pro Gly Thr Gly Ala Ile Arg Gln Gly Ala Asn
189 225                 230                 235                 240
191 Met Lys Gly Ala Ile Thr Leu Thr Ile Leu Ile Gly Val Phe Val Val
192             245                 250                 255
194 Cys Trp Ala Pro Phe Phe Leu His Leu Ile Phe Tyr Ile Ser Cys Pro
195             260                 265                 270
197 Gln Asn Pro Tyr Cys Val Cys Phe Met Ser His Phe Asn Leu Tyr Leu
198     275                 280                 285
200 Ile Leu Ile Met Cys Asn Ser Ile Ile Asp Pro Leu Ile Tyr Ala Leu
201     290                 295                 300
203 Arg Ser Gln Glu Leu Arg Lys Thr Phe Lys Glu Ile Ile Ser Ser Tyr
204 305                 310                 315                 320
206 Pro Leu Gly Gly Leu Cys Asp Leu Ser Ser Arg Tyr
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               RAW SEQUENCE LISTING              DATE: 10/02/2002
               PATENT APPLICATION: US/10/074,754   TIME: 09:45:54

               Input Set : A:\96886-L.seq.txt
               Output Set: N:\CRF4\10022002\J074754.raw
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  213 <213> ORGANISM: Artificial Sequence
  215 <220> FEATURE:
  216 <223> OTHER INFORMATION: Description of Artificial Sequence: degenerate
  217      oligonucleotide primer
  219 <220> FEATURE:
  220 <221> NAME/KEY: misc_feature
  221 <222> LOCATION: (23)..(24)
  222 <223> OTHER INFORMATION: "n" is inosine
  224 <400> SEQUENCE: 3
  225 gagtcgacct gtgygysaty rcnnntkgacm gstac              35
  228 <210> SEQ ID NO: 4
  229 <211> LENGTH: 32
  230 <212> TYPE: DNA
  231 <213> ORGANISM: Artificial Sequence
  233 <220> FEATURE:
  234 <223> OTHER INFORMATION: Description of Artificial Sequence: degenerate
  235      oligonucleotide primer
  237 <220> FEATURE:
  238 <221> NAME/KEY: misc_feature
  239 <222> LOCATION: (18)
  240 <223> OTHER INFORMATION: "n" is inosine
  242 <400> SEQUENCE: 4
  243 cagaattcag wagggcancc agcagasryg aa              32
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  247 <211> LENGTH: 7
  248 <212> TYPE: PRT
  249 <213> ORGANISM: Artificial Sequence
  251 <220> FEATURE:
  252 <221> NAME/KEY: SITE
  253 <222> LOCATION: (1)
  254 <223> OTHER INFORMATION: "Xaa" is norleucine
  256 <220> FEATURE:
  257 <221> NAME/KEY: SITE
  258 <222> LOCATION: (4)
  259 <223> OTHER INFORMATION: "Xaa" is naphthyl-D-alanine
  261 <220> FEATURE:
  262 <223> OTHER INFORMATION: Description of Artificial Sequence: peptide
  263      cyclized between the epsilon amino group of the
  264      lysine and the sidechain carboxyl group of the
  265      aspartic acid
  267 <400> SEQUENCE: 5
  268 Xaa Asp His Xaa Arg Trp Lys
  269  1             .    5
  272 <210> SEQ ID NO: 6
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274 <212> TYPE: DNA
275 <213> ORGANISM: Artificial Sequence
277 <220> FEATURE:
278 <223> OTHER INFORMATION: Description of Artificial Sequence: degenerate
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281 <400> SEQUENCE: 6
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286 <211> LENGTH: 48
287 <212> TYPE: DNA
288 <213> ORGANISM: Artificial Sequence
290 <220> FEATURE:
291 <223> OTHER INFORMATION: Description of Artificial Sequence:
292      oligonucleotide primer
294 <400> SEQUENCE: 7
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299 <211> LENGTH: 48
300 <212> TYPE: DNA
301 <213> ORGANISM: Artificial Sequence
303 <220> FEATURE:
304 <223> OTHER INFORMATION: Description of Artificial Sequence:
305      oligonucleotide primer
307 <400> SEQUENCE: 8
308 ccgaagcccg cctaatgagc gggctttttt ttgcatactg cggccgct             48
311 <210> SEQ ID NO: 9
312 <211> LENGTH: 72
313 <212> TYPE: DNA
314 <213> ORGANISM: Artificial Sequence
316 <220> FEATURE:
317 <223> OTHER INFORMATION: Description of Artificial Sequence:
318      oligonucleotide primer
320 <400> SEQUENCE: 9
321 ggccggcatg catcaagctt atctcgagat cgtcgactac catggtacat cgatcaggta  60
323 ccatcccggg gc                                               72
326 <210> SEQ ID NO: 10
327 <211> LENGTH: 72
328 <212> TYPE: DNA
329 <213> ORGANISM: Artificial Sequence
331 <220> FEATURE:
332 <223> OTHER INFORMATION: Description of Artificial Sequence:
333      oligonucleotide primer
335 <400> SEQUENCE: 10
336 ggccgcccccg ggatggtacc tgatcgatgt accatggtag tcgacgatct cgagataagc  60
338 ttgatgcatg cc                                               72
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 10/02/2002
PATENT APPLICATION: US/10/074,754   TIME: 09:45:55

Input Set : A:\96886-L.seq.txt
Output Set: N:\CRF4\10022002\J074754.raw

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 23,24
Seq#:4; N Pos. 18
Seq#:5; Xaa Pos. 1,4

Invalid Line Length:
The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23
Seq#:1; Line(s) 24,25,26,27,28,29,30,31,32,33,34,35,36,37,38,39,40,41,42,43
Seq#:1; Line(s) 44,45,46,47,48,49,50,51,52,53,54,55,56,57,58,59,60,61,62,63
Seq#:1; Line(s) 64,65,66,67,68,69,70,71,72,73,74,75,76,77,78,79,80,81,82,83
Seq#:1; Line(s) 84,85,86,87,88,89,90,91,92,93,94,95,96,97,98,99,100,101,102
Seq#:1; Line(s) 103,104,105,106,107,108,109,110,111,112,113,114,115,116,117
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Seq#:1; Line(s) 133,134,135,136,137,138,139,140
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Seq#:3; Line(s) 226,227,228
Seq#:4; Line(s) 229,230,231,232,233,234,235,236,237,238,239,240,241,242,243
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